Database :   UniProt_02:*
                  1: uniprot_sprot:*
                  2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1328	99.6	<u>349</u>	1	GUB_FIBSU	P17989 fibrobacter
2	266.5	20.0	259	1	GUB_BACBR	P37073 bacillus br
3	266.5	20.0	851	2	Q9K7X5	Q9k7x5 bacillus ha
4	248.5	18.6	256	2	Q9APD8	Q9apd8 bacillus ci
5	247.5	18.6	276	2	Q45648	Q45648 bacillus sp
6	245.5	18.4	214	2	Q8GMY0	Q8gmy0 bacillus li
7	245.5	18.4	242	1	GUB_BACSU	P04957 bacillus su
8	244.5	18.3	215	2	Q84GK1	Q84gk1 bacillus li
9	243	18.2	334	2	Q84C00	Q84c00 clostridium
10	242.5	18.2	214	2	Q93GE8	Q93ge8 uncultured
11	242.5	18.2	802	1	XYND_RUMFL	Q53317 ruminococcu
12	242.5	18.2	802	2	Q9S310	Q9s310 ruminococcu
13	241.5	18.1	214	2	Q93GE7	Q93ge7 uncultured

```
Database :        PIR_79:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*


    Pred. No. is the number of results predicted by chance to have a
    score greater than or equal to the score of the result being printed,
    and is derived by analysis of the total score distribution.

                                    SUMMARIES
                        %
Result              Query
    No.    Score   Match Length DB   ID                    Description
--------------------------------------------------------------------------------
      1     1328    99.6     349  2   A44507               licheninase (EC 3.
      2    266.5    20.0     851  2   H84053               endo-beta-1,3-1,4
      3    265.5    19.9     252  2   A48378               licheninase (EC 3.
      4    247.5    18.6     276  2   I40453               licheninase (EC 3.
      5    245.5    18.4     242  1   LXBS                 licheninase (EC 3.
      6    242.5    18.2     802  2   A36910               xylanase, beta(1,3
      7    238.5    17.9     239  1   A29091               licheninase (EC 3.
      8      237    17.8     334  1   S23498               licheninase (EC 3.
      9    229.5    17.2     243  1   S15388               licheninase (EC 3.
     10      226    17.0     237  1   S11927               licheninase (EC 3.
     11      225    16.9     238  1   S19012               licheninase (EC 3.
```

```
Database :        Issued_Patents_AA:*
                  1:  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2:  /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*


       Pred. No. is the number of results predicted by chance to have a
       score greater than or equal to the score of the result being printed,
       and is derived by analysis of the total score distribution.

                                    SUMMARIES
```

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1103	82.7	228	3	US-09-286-690-12	Sequence 12, Appl
2	257.5	19.3	308	4	US-09-463-862A-1	Sequence 1, Appli
3	245.5	18.4	242	3	US-09-286-690-8	Sequence 8, Appli
4	244	18.3	239	1	US-08-103-998-2	Sequence 2, Appli
5	231.5	17.4	279	3	US-09-286-690-9	Sequence 9, Appli
6	229.5	17.2	243	3	US-09-286-690-10	Sequence 10, Appl
7	225	16.9	238	3	US-09-286-690-7	Sequence 7, Appli
8	222.5	16.7	242	3	US-09-286-690-11	Sequence 11, Appl
9	220.5	16.5	237	1	US-08-103-998-4	Sequence 4, Appli
10	200.5	15.0	526	4	US-09-248-796A-14807	Sequence 14807, A
11	189	14.2	245	3	US-09-286-690-2	Sequence 2, Appli
12	185	13.9	462	4	US-09-248-796A-14808	Sequence 14808, A

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	257.5	19.3	308	2	AAW93001	Aaw93001 B. alkalo
2	246.5	18.5	242	1	AAP95000	Aap95000 Bacillus
3	244	18.3	214	4	AAE07317	Aae07317 Barley re
4	244	18.3	239	2	AAR06621	Aar06621 Hybrid (1
5	230	17.3	212	5	ABP58995	Abp58995 Paenibaci
6	226	17.0	234	2	AAR03775	Aar03775 Thermosta
7	226	17.0	237	2	AAR05803	Aar05803 Heat-stab
8	225	16.9	208	5	ABB76858	Abb76858 Bacterial
9	225	16.9	214	5	ABB76859	Abb76859 Bacterial
10	220.5	16.5	237	2	AAR06622	Aar06622 Hybrid (1
11	204.5	15.3	504	8	ADP98858	Adp98858 C. albica
12	189	14.2	245	2	AAW37884	Aaw37884 Lichenase
13	185	13.9	453	7	ADC01836	Adc01836 C. albica
14	185	13.9	453	8	ADP98992	Adp98992 C. albica

```
Database :        PIR_79:*
                1:  pir1:*
                2:  pir2:*
                3:  pir3:*
                4:  pir4:*
```

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

<div align="center">SUMMARIES</div>

Result No.	Score	% Query Match	Length	DB	ID	Description
1	2020.5	70.5	720	2	T52564	Mre11 protein homo
2	852.5	29.8	649	1	S58097	probable dna repai
3	768	26.8	692	1	S57592	probable phosphoes
4	724	25.3	772	2	T27512	hypothetical prote
5	178	6.2	443	1	G69378	probable phosphoes
6	175.5	6.1	423	2	E75103	phosphoesterase ho
7	174.5	6.1	413	1	D71083	probable phosphoes
8	163.5	5.7	587	1	E69171	phosphoesterase-re
9	150.5	5.3	381	2	C90395	DNA repair protein
10	143	5.0	1038	2	JC5497	claustrin - chicke
11	141.5	4.9	409	2	E72765	probable phosphoes
12	136	4.7	1957	2	T38077	hypothetical coile

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Database :        Issued_Patents_AA:*
                  1:  /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
                  2:  /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
                  3:  /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
                  4:  /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
                  5:  /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
                  6:  /cgn2_6/ptodata/1/iaa/backfiles1.pep:*


      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                                    SUMMARIES
                        %
Result             Query
   No.    Score   Match Length DB   ID                      Description
-------------------------------------------------------------------------------
     1    2864   100.0    552   4   US-09-835-654-2         Sequence 2, Appli
     2  2020.5    70.5    720   3   US-09-480-921B-8        Sequence 8, Appli
     3   954.5    33.3    680   4   US-09-538-092-1165      Sequence 1165, Ap
     4     768    26.8    692   4   US-09-538-092-632       Sequence 632, App
     5   507.5    17.7    270   4   US-09-248-796A-19151    Sequence 19151, A
     6   141.5     4.9    132   4   US-09-270-767-33195     Sequence 33195, A
     7   141.5     4.9    132   4   US-09-270-767-48412     Sequence 48412, A
     8     136     4.7    857   4   US-09-248-796A-20522    Sequence 20522, A
     9     122     4.3   1120   3   US-09-147-404-1         Sequence 1, Appli
    10     122     4.3   1935   4   US-09-538-092-916       Sequence 916, App
```